

SEQUENCE LISTING

<110> Duvick, Jonathan P.
 Gilliam, Jacob T.
 Maddox, Joyce R.
 Crasta, Oswald R.
 Folkerts, Otto

<120> Amino Polyol Amine Oxidase
 Polynucleotides and Related Polypeptides and Methods of Use

<130> 0875C

<150> US 60/092,936
<151> 1998-07-15

<150> US 09/352,168
<151> 1999-07-12

<160> 33

<170> FastSEQ for Windows Version 3.0

<210> 1
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<212> DNA
<213> Exophiala spinifera.

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<222> (346)...(346)
<223> n = A,T,C or G

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attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatggggtca cagctcgatt	240
ggaggacgcc cgagaagcc ttttcgcgcc accacggct gtcccatacg aagactatct	300
tgcataatgt gcccaggata gaattttccg ccaatgcttg cttctcgccg ggaagaggtg	360
gtgaaaatgt caaggtggg tacaagggttgc tggttaacgaa accancacc ttttgcttc	372
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tacaagggttgc tggttaacgaa accaccacc ttttgcttc ggaacacggc gcccggggcc	180
gatcgtaactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc	182
ac	

<210> 3
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<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 3' RACE, N21965

<400> 3
tggtttcgtt accgacaacc ttgtatccc 29

<210> 4
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide for 5' RACE, N21968

<400> 4
gagttggtcc cagacagact tttgtcgt 28

<210> 5
<211> 1389
<212> DNA
<213> Exophiala spinifera

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<222> (1)...(1386)

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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
20 25 30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
35 40 45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
50 55 60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65 70 75 80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
85 90 95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
100 105 110

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc 384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
115 120 125

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg 432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
130 135 140

ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu 145 150 155 160	480
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly 165 170 175	528
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys 180 185 190	576
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly 195 200 205	624
cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met 210 215 220	672
tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala 225 230 235 240	720
gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly 245 250 255	768
gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu 260 265 270	816
tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala 275 280 285	864
ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val 290 295 300	912
tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln 305 310 315 320	960
tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val 325 330 335	1008
gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg 340 345 350	1056
aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp 355 360 365	1104
caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro 370 375 380	1152
gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly	1200

385	390	395	400	
gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser 405				1248
gct ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr 420				1296
tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln 435				1344
cga ggt got gca gaa gtt gtg gct agc ctg gtg cca gca gca Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 450				1386
tag				1389
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Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
 290 295 300
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
 305 310 315 320
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
 325 330 335
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
 340 345 350
 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
 355 360 365
 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
 370 375 380
 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
 385 390 395 400
 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
 405 410 415
 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
 420 425 430
 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
 435 440 445
 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 7
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 <212> DNA
 <213> Exophiala spinifera

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 <222> (1) ... (646)

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 <221> CDS
 <222> (700) ... (1439)

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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
 20 25 30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144
 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45

ccc ggc agg acg act atc aac gac ctc ggc gct ggc tgg atc aat gac 192
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His His Gln Ala Gln Asp
 85 90 95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu 100 105 110	336
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile 115 120 125	384
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg 130 135 140	432
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu 145 150 155 160	480
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly 165 170 175	528
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys 180 185 190	576
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly 195 200 205	624
cag tat gtg cga tgc aaa aca g gtgcgtgtgg tgtcgtctca ggtgggggac Gln Tyr Val Arg Cys Lys Thr 210 215	676
tgcgttctca gtggcatttc cag gt atg cag tcg att tgc cat gcc atg tca Gly Met Gln Ser Ile Cys His Ala Met Ser 220 225	728
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu 230 235 240	776
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala 245 250 255	824
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr 260 265 270	872
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu 275 280 285	920
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp 290 295 300 305	968
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser 310 315 320	1016
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat	1064

Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp			
325	330	335	
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cg aag			1112
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys			
340	345	350	
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa			1160
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln			
355	360	365	
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc			1208
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala			
370	375	380	385
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct			1256
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala			
390	395	400	
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg			1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala			
405	410	415	
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct			1352
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser			
420	425	430	
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga			1400
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg			
435	440	445	
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Gly Ala Ala Glu Val Ala Ser Leu Val Pro Ala Ala			
450	455	460	
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<211> 462			
<212> PRT			
<213> Exophiala spinifera			
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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly			
35	40	45	
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp			
50	55	60	
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu			
65	70	75	80
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp			
85	90	95	
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu			
100	105	110	
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile			
115	120	125	
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg			
130	135	140	
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu			
145	150	155	160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
 165 170 175
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
 180 185 190
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
 195 200 205
 Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
 210 215 220
 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
 225 230 235 240
 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
 245 250 255
 Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu
 260 265 270
 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
 275 280 285
 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
 290 295 300
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
 305 310 315 320
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
 325 330 335
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
 340 345 350
 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
 355 360 365
 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
 370 375 380
 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
 385 390 395 400
 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
 405 410 415
 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
 420 425 430
 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
 435 440 445
 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

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 <212> PRT
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<400> 9

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 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95
 Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110
 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
 115 120 125
 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg

130	135	140
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu		
145	150	155
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly		160
165	170	175
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys		
180	185	190
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly		
195	200	205
Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly		
210	215	220
Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met		
225	230	235
Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro		240
245	250	255
Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro		
260	265	270
Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln		
275	280	285
Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys		
290	295	300
His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr		
305	310	315
Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn		320
325	330	335
Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser		
340	345	350
Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly		
355	360	365
Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr		
370	375	380
Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg		
385	390	395
Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu		400
405	410	415
Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg		
420	425	430
Ser Glu Arg Arg Ser Arg Val Phe Ile Ser Leu Glu Arg Arg Arg Leu		
435	440	445
Phe Gly Lys Gly Ile Trp Lys Gly Pro Tyr		
450	455	

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<211> 1392
<212> DNA
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<220>
<221> CDS
<222> (1)...(1389)

<221> misc_feature
<222> (1)...(3)
<223> Extra lysine in K:trAPAO

<400> 10

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Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly		
1	5	10
		15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt		96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val		

20	25	30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	35	40	144
45			
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	50	55	192
55		60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	65	70	240
75		80	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	85	90	288
95			
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	100	105	336
110			
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	115	120	384
125			
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	130	135	432
140			
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	145	150	480
155		160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	165	170	528
175			
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	180	185	576
190			
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	195	200	624
205			
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	210	215	672
220			
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	225	230	720
235		240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	245	250	768
255			
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	260	265	816
270			

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285	864
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290 295 300	912
gta tgg gac aag ccg tgg tgg cgcc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305 310 315 320	960
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335	1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340 345 350	1056
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355 360 365	1104
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370 375 380	1152
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 385 390 395 400	1200
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 405 410 415	1248
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 420 425 430	1296
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 435 440 445	1344
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 450 455 460	1389
tag	1392
<210> 11	
<211> 463	
<212> PRT	
<213> Exophiala spinifera	
<220>	
<223> Extra lysine in the polypeptide sequence of K:trAPAO, 463 aa.	
<400> 11	
Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly 1 5 10 15	

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95
 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
 165 170 175
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 180 185 190
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
 195 200 205
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
 210 215 220
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
 225 230 235 240
 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
 245 250 255
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
 260 265 270
 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 275 280 285
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 290 295 300
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 305 310 315 320
 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 325 330 335
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 340 345 350
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 355 360 365
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 370 375 380
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 385 390 395 400
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 405 410 415
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 420 425 430
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 12
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer sequence designed for cloning DNA into
 expression vectors, N23256

<400> 12
 ggggaattca aagacaacgt tgccggacgtg gtag

34

<210> 13
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer sequence designed for cloning DNA into
 expression vectors, N23259

<400> 13
 ggggcggccg cctatgctgc tggcaccagg ctag

34

<210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 3' RACE, N21965

<400> 14
 tggtttcgtt accgacaacc ttgttatccc

29

<210> 15
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 5' race, N21968

<400> 15
 gagtttgtcc cagacagact tttgtcgt

28

<210> 16
 <211> 1673
 <212> DNA
 <213> Exophiala spinifera

<220>
 <221> sig_peptide
 <222> (1)...(267)
 <223> yeast alpha mating factor secretion signal.

<221> CDS
 <222> (1)...(1662)

<400> 16
 atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser

-85 -80 -75

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa
 Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln

-70 -65 -60

48

96

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe -55 -50 -45	144
gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu -40 -35 -30	192
ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val -25 -20 -15 -10	240
tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala -5 1 5	288
gac gtg gta gtg gtc ggc gct ggc ttg agc ggt ttg gag acg gca cgc Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg 10 15 20	336
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp 25 30 35	384
cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr 40 45 50 55	432
act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser 60 65 70	480
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln 75 80 85	528
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr 90 95 100	576
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala 105 110 115	624
ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser 120 125 130 135	672
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val 140 145 150	720
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu 155 160 165	768
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His 170 175 180	816
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt	864

Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly			
185	190	195	
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga			912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg			
200	205	210	215
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt			960
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu			
220	225	230	
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag			1008
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln			
235	240	245	
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga			1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg			
250	255	260	
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg			1104
Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu			
265	270	275	
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat			1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn			
280	285	290	295
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg			1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro			
300	305	310	
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac			1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp			
315	320	325	
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg			1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp			
330	335	340	
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa			1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln			
345	350	355	
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca			1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala			
360	365	370	375
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc			1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu			
380	385	390	
gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc			1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala			
395	400	405	
gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg			1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr			
410	415	420	
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg			1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp			
425	430	435	

aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca
 Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
 440 445 450 455
 gaa gtt gtc gct agc ctg gtc cca gca gca taggcggccg c
 Glu Val Val Ala Ser Leu Val Pro Ala Ala
 460 465
 1632

<210> 17
 <211> 554
 <212> PRT
 <213> Exophiala spinifera

<220>
 <221> SIGNAL
 <222> (1)...(89)
 <223> yeast alpha mating factor secretion signal.

<400> 17
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
 -85 -80 -75
 Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln
 -70 -65 -60
 Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
 -55 -50 -45
 Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
 -40 -35 -30
 Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
 -25 -20 -15 -10
 Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
 -5 1 5
 Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
 10 15 20
 Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
 25 30 35
 Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
 40 45 50 55
 Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
 60 65 70
 Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
 75 80 85
 Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
 90 95 100
 Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
 105 110 115
 Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
 120 125 130 135
 Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
 140 145 150
 Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
 155 160 165
 Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
 170 175 180
 Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly
 185 190 195
 Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
 200 205 210 215
 Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
 220 225 230
 Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln

235	240	245
Ser Ala Ser Gly Cys Thr Val Arg	Ser Ala Ser Gly Ala Val Phe Arg	
250	255	260
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu		
265	270	275
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn		
280	285	290
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro		295
300	305	310
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp		
315	320	325
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp		
330	335	340
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln		
345	350	355
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala		
360	365	370
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu		375
380	385	390
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala		
395	400	405
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr		
410	415	420
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp		
425	430	435
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala		
440	445	450
Glu Val Val Ala Ser Leu Val Pro Ala Ala		455
460	465	

<210> 18
<211> 2079
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (1)...(2076)

<223> GST:K:trAPAO 2079 nt. Translation starting at nt 1
- 687, gst fusion + polylinker; 688-2076,
K:trAPAO; 2077-2079, stop codon. For bacterial
expression.

<221> misc_feature
<222> (1)...(687)
<223> gst fusion + polylinker

<221> misc_feature
<222> (688)...(2076)
<223> K:trAPAO

<221> misc_feature
<222> (688)...(690)
<223> Extra lysine

<400> 18

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

48

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg

96

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu			
20	25	30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg			144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu			
35	40	45	
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa			192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys			
50	55	60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac			240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn			
65	70	75	80
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa			288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu			
85	90	95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt			336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser			
100	105	110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa			384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu			
115	120	125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat			432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn			
130	135	140	
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat			480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp			
145	150	155	160
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta			528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu			
165	170	175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac			576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr			
180	185	190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc			624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala			
195	200	205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt			672
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg			
210	215	220	
gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc			720
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Gly			
225	230	235	240
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt			768
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly			
245	250	255	
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act			816
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr			
260	265	270	

ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly 275 280 285	864
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe 290 295 300	912
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser 305 310 315 320	960
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac Ile His Gln Ala Gln Asp Gly Thr Thr Ala Pro Tyr Gly Asp 325 330 335	1008
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro 340 345 350	1056
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala 355 360 365	1104
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys 370 375 380	1152
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile 385 390 395 400	1200
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt Thr Arg Ala Leu Leu Gly Val Ala His Glu Ile Ser Met Leu Phe 405 410 415	1248
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser 420 425 430	1296
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag Asp Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln 435 440 445	1344
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His 450 455 460	1392
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgc tgt aca Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr 465 470 475 480	1440
gta cga tcg gcc tcg ggc ttc cga agc aaa aag gtg gtg gtt Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val 485 490 495	1488
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu 500 505 510	1536
ccc gcc gag aag caa gca ttg ggc gaa aat tct atc ctg ggc tac tat	1584

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr			
515	520	525	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc			1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly			
530	535	540	
ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga			1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg			
545	550	555	560
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg			1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met			
565	570	575	
gtc gga gac ccg gga cg aag tgg tcc caa cag tcc aag cag gta cga			1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg			
580	585	590	
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg			1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly			
595	600	605	
gcc caa gtc cca gag ccg aac gtg ctc gaa atc gag tgg tcg aag			1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys			
610	615	620	
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat			1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp			
625	630	635	640
ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat			1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His			
645	650	655	
ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg			2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly			
660	665	670	
gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg			2064
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu			
675	680	685	
gtg cca gca gca tag			2079
Val Pro Ala Ala			
690			
<210> 19			
<211> 692			
<212> PRT			
<213> Unknown			
<220>			
<223> GST:K:trAPAO; GST + linker, aa 1-229; K:trAPAO, aa			
230-692			
<400> 19			
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro			
1	5	10	15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu			
20	25	30	

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Gly
 225 230 235 240
 Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
 245 250 255
 Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
 260 265 270
 Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
 275 280 285
 Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
 290 295 300
 Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
 305 310 315 320
 Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp
 325 330 335
 Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro
 340 345 350
 Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
 355 360 365
 Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
 370 375 380
 Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
 385 390 395 400
 Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
 405 410 415
 Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
 420 425 430
 Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
 435 440 445
 Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
 450 455 460
 Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
 465 470 475 480
 Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
 485 490 495
 Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
 500 505 510
 Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
 515 520 525

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
 530 535 540
 Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
 545 550 555 560
 Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
 565 570 575
 Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
 580 585 590
 Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
 595 600 605
 Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
 610 615 620
 Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
 625 630 635 640
 Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
 645 650 655
 Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
 660 665 670
 Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
 675 680 685
 Val Pro Ala Ala
 690

<210> 20
 <211> 1464
 <212> DNA
 <213> Unknown

<220>
 <221> sig_peptide
 <222> (1)...(72)
 <223> Barley Alpha Amylase signal sequence.

<221> misc_feature
 <222> (73)...(1464)
 <223> K:trAPAOcDNA

<221> CDS
 <222> (1)...(1461)

<223> Nucleotide sequence of K:trAPAO translational fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize. Nucleotides 1-72, barley alpha amylase signal sequence, nucleotides 73-75, added lysine residue; nucleotides 76 -1464 , trAPAO cDNA.

<221> misc_feature
 <222> (73)...(75)
 <223> Added lysine residue

<400> 20

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly		
-20	-15	-10

ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta
 Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val

-5	1	5	96
----	---	---	----

gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag
 Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln

			144
--	--	--	-----

10	15	20	
gcc gcc ggt ctg tcc tgc ctc gtt ctt gag ggc atg gat cgt gta ggg Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly			
25	30	35	40
gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn			
45	50	55	240
gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser			
60	65	70	288
aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr			
75	80	85	336
gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro			
90	95	100	384
tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu			
105	110	115	432
ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac Leu Leu Pro Val Trp Ser Gln Leu Ile Glu His Ser Leu Gln Asp			
125	130	135	480
ctc aag gcg agc cct cag gcg aag cggt ctc gac agt gtg agc ttc gcg Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala			
140	145	150	528
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala			
155	160	165	576
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser			
170	175	180	624
atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn			
185	190	195	672
att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr			
205	210	215	720
ggc atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly			
220	225	230	768
tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser			
235	240	245	816
ggc tgt aca gta cga tcg gcc tcg ggc ggc gtg ttc cga agc aaa aag Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys			
250	255	260	864

gtg gtt ttc ccc acc ttg tat ccc acc ttg aca ttt tca Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser 265 270 275 280	912
cca cct ctt ccc gag aag caa gca ttg gcg gaa aat tct atc ctg Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu 285 290 295	960
ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg 300 305 310	1008
gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser 315 320 325	1056
ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr 330 335 340	1104
tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys 345 350 355 360	1152
cag gta cga caa aag tct gtc tgg gac caa ctc ccg gca gcc tac gag Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu 365 370 375	1200
aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu 380 385 390	1248
tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly 395 400 405	1296
ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys 410 415 420	1344
agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr 425 430 435 440	1392
atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val 445 450 455	1440
gct agc ctg gtg cca gca gca tag Ala Ser Leu Val Pro Ala Ala 460	1464

<210> 21
<211> 487
<212> PRT
<213> Unknown

<220>
<221> SIGNAL
<222> (1)...(24)

<223> K:trAPAO translational fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize.

<400> 21

Met	Ala	Asn	Lys	His	Leu	Ser	Leu	Ser	Leu	Phe	Leu	Val	Leu	Leu	Gly
					-20					-15					-10
Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Lys	Asp	Asn	Val	Ala	Asp	Val	Val
					-5					1					5
Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln
					10				15					20	
Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly
					25				30			35		40	
Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn
					45				50					55	
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser
					60				65					70	
Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr
					75				80					85	
Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro
					90				95					100	
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu
					105				110			115		120	
Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp
					125				130					135	
Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala
					140				145					150	
His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala
					155				160					165	
Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser
					170				175					180	
Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn
					185				190			195		200	
Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr
					205				210					215	
Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly
					220				225					230	
Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser
					235				240					245	
Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys
					250				255					260	
Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser
					265				270			275		280	
Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu
					285				290					295	
Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg
					300				305					310	
Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser
					315				320					325	
Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr
					330				335					340	
Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys
					345				350			355		360	
Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu
					365				370					375	
Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu
					380				385					390	
Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly
					395				400					405	
Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys
					410				415					420	
Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr

425 430 435 440 Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val 445 450 455 Ala Ser Leu Val Pro Ala Ala 460	
<p><210> 22 <211> 1803 <212> DNA <213> Exophiala spinifera</p> <p><220> <221> CDS <222> (1)...(1800)</p>	
<p><400> 22</p>	
atg gca ctt gca ccc agc tac atc aat ccc cca aac gtc gcc tcc cca Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro 1 5 10 15	48
<p>gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Arg Tyr Val 20 25 30</p>	
aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro 35 40 45	144
<p>gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys 50 55 60</p>	
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr 65 70 75 80	240
<p>tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly 85 90 95</p>	
ctg aag gct acc ttt gcc ctt gac agg ctc cct tgc acg ctg gtg Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val 100 105 110	336
<p>cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala 115 120 125</p>	
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val 130 135 140	432
<p>gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 145 150 155 160 </p>	
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 165 170 175	528
<p>ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile</p>	
	576

180	185	190	
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 195	200	205	624
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 210	215	220	672
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 225	230	235	720
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 245	250	255	768
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 260	265	270	816
gac ctc aag gcg agc cct cag gcg aag cggt ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 275	280	285	864
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 290	295	300	912
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 305	310	315	960
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 325	330	335	1008
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 340	345	350	1056
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 355	360	365	1104
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 370	375	380	1152
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtt ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 385	390	395	1200
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 405	410	415	1248
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 420	425	430	1296

ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp 435 440 445	1344
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 450 455 460	1392
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 465 470 475 480	1440
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 485 490 495	1488
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 500 505 510	1536
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 515 520 525	1584
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 530 535 540	1632
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 545 550 555 560	1680
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 565 570 575	1728
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val 580 585 590	1776
gtg gct agc ctg gtg cca gca gca tag Val Ala Ser Leu Val Pro Ala Ala 595 600	1803

<210> 23
<211> 600
<212> PRT
<213> Exophiala spinifera

<400> 23

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro 1 5 10 15	
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val 20 25 30	
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro 35 40 45	
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys 50 55 60	
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr 65 70 75 80	
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	

85	90	95
Leu Lys Ala Thr Phe Ala Leu Asp Arg	Leu Pro Pro Cys	Thr Leu Val
100	105	110
Pro Val Ser Ala Leu Ser Ser Pro	Glu Tyr Leu Phe Glu Val Asp Ala	
115	120	125
Thr Ala Leu Val Pro Gly His	Thr Thr Pro Asp Asn Val Ala Asp Val	
130	135	140
Val Val Val Gly Ala Gly	Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
145	150	155
Gln Ala Ala Gly	Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
165	170	175
Gly Gly Lys Thr Leu Ser Val Gln	Ser Gly Pro Gly Arg Thr Thr Ile	
180	185	190
Asn Asp Leu Gly Ala Ala Trp	Ile Asn Asp Ser Asn Gln Ser Glu Val	
195	200	205
Ser Arg Leu Phe Glu Arg	Phe His Leu Glu Gly Glu Leu Gln Arg Thr	
210	215	220
Thr Gly Asn Ser Ile His	Gln Ala Gln Asp Gly Thr Thr Thr Ala	
225	230	235
Pro Tyr Gly Asp Ser	Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala	
245	250	255
Glu Leu Leu Pro Val Trp Ser Gln	Leu Ile Glu Glu His Ser Leu Gln	
260	265	270
Asp Leu Lys Ala Ser Pro Gln	Ala Lys Arg Leu Asp Ser Val Ser Phe	
275	280	285
Ala His Tyr Cys Glu Lys	Glu Leu Asn Leu Pro Ala Val Leu Gly Val	
290	295	300
Ala Asn Gln Ile Thr Arg	Ala Leu Leu Gly Val Glu Ala His Glu Ile	
305	310	315
Ser Met Leu Phe Leu Thr Asp Tyr	Ile Lys Ser Ala Thr Gly Leu Ser	
325	330	335
Asn Ile Phe Ser Asp Lys Lys	Asp Gly Gly Gln Tyr Met Arg Cys Lys	
340	345	350
Thr Gly Met Gln Ser Ile Cys	His Ala Met Ser Lys Glu Leu Val Pro	
355	360	365
Gly Ser Val His Leu Asn Thr	Pro Val Ala Glu Ile Glu Gln Ser Ala	
370	375	380
Ser Gly Cys Thr Val Arg	Ser Ala Ser Gly Ala Val Phe Arg Ser Lys	
385	390	395
Lys Val Val Val Ser	Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	
405	410	415
Ser Pro Pro Leu Pro Ala Glu	Lys Gln Ala Leu Ala Glu Asn Ser Ile	
420	425	430
Leu Gly Tyr Tyr Ser Lys	Ile Val Phe Val Trp Asp Lys Pro Trp Trp	
435	440	445
Arg Glu Gln Gly Phe Ser	Gly Val Leu Gln Ser Ser Cys Asp Pro Ile	
450	455	460
Ser Phe Ala Arg Asp	Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
465	470	475
Thr Cys Phe Met Val	Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
485	490	495
Lys Gln Val Arg Gln	Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
500	505	510
Glu Asn Ala Gly Ala Gln	Val Pro Glu Pro Ala Asn Val Leu Glu Ile	
515	520	525
Glu Trp Ser Lys Gln Gln	Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
530	535	540
Gly Leu Asn Asp Leu Ile	Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
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Lys Ser Val His Phe Val	Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
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Tyr Met Glu Gly Ala Ile Arg Ser	Gly Gln Arg Gly Ala Ala Glu Val	

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cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt
 Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly 336
 75 80 85

 gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag
 Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu 384
 90 95 100

 aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa
 Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu 432
 105 110 115 120

 tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc 480
 Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala
 125 130 135

 aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg 528
 Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu
 140 145 150

 ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg 576
 Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly
 155 160 165

 ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca 624
 Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala
 170 175 180

 gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg 672
 Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala
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 Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro
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 ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc 768
 Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe
 220 225 230

 ccc aag gga gat ttg tcc gaa cct tgg aac acc act gttcaa gct ctc 816
 Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu
 235 240 245

 aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat 864
 Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp
 250 255 260

 ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag 912
 Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu
 265 270 275 280

 tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc 960
 Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg
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 acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc 1008
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att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile 365 370 375			1200
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tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val 395 400 405			1296
tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala 410 415 420			1344
agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala 425 430 435 440			1392
tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln 445 450 455			1440
gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val 460 465 470			1488
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tat tat act gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly 490 495 500			1584
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act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 605 610 615	1920
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 620 625 630	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 635 640 645	2016
gac ctc aag gcg agc cct cag gcg aag cggt ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 650 655 660	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 665 670 675 680	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685 690 695	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 700 705 710	2208
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 715 720 725	2256
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 730 735 740	2304
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 745 750 755 760	2352
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 765 770 775	2400
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 780 785 790	2448
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 795 800 805	2496
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	2544

810

815

820

cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 825 830 835 840	2592
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 845 850 855	2640
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 860 865 870	2688
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gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 890 895 900	2784
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 905 910 915 920	2832
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 925 930 935	2880
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aat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val 955 960 965	2976
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<213> Unknown

<220>
<221> SIGNAL
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Gly Met Val Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
10 15 20
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
25 30 35 40
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr

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Arg	Glu	Ile	Thr	Met	Ala	Trp	Phe	Asn	Thr	Pro	Pro	Pro	Ser	Ala	Gly
			75				80				85				
Glu	Ser	Glu	Asp	Cys	Leu	Asn	Leu	Asn	Ile	Tyr	Val	Pro	Gly	Thr	Glu
			90			95				100					
Asn	Thr	Asn	Lys	Ala	Val	Met	Val	Trp	Ile	Tyr	Gly	Gly	Ala	Leu	Glu
			105		110				115				120		
Tyr	Gly	Trp	Asn	Ser	Phe	His	Leu	Tyr	Asp	Gly	Ala	Ser	Phe	Ala	Ala
			125				130				135				
Asn	Gln	Asp	Val	Ile	Ala	Val	Thr	Ile	Asn	Tyr	Arg	Thr	Asn	Ile	Leu
			140			145				150					
Gly	Phe	Pro	Ala	Ala	Pro	Gln	Leu	Pro	Ile	Thr	Gln	Arg	Asn	Leu	Gly
			155			160				165					
Phe	Leu	Asp	Gln	Arg	Phe	Ala	Leu	Asp	Trp	Val	Gln	Arg	Asn	Ile	Ala
			170			175				180					
Ala	Phe	Gly	Gly	Asp	Pro	Arg	Lys	Val	Thr	Ile	Phe	Gly	Gln	Ser	Ala
			185		190				195			200			
Gly	Gly	Arg	Ser	Val	Asp	Val	Leu	Leu	Thr	Ser	Met	Pro	His	Asn	Pro
			205				210				215				
Pro	Phe	Arg	Ala	Ala	Ile	Met	Glu	Ser	Gly	Val	Ala	Asn	Tyr	Asn	Phe
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Pro	Lys	Gly	Asp	Leu	Ser	Glu	Pro	Trp	Asn	Thr	Thr	Val	Gln	Ala	Leu
			235			240				245					
Asn	Cys	Thr	Thr	Ser	Ile	Asp	Ile	Leu	Ser	Cys	Met	Arg	Arg	Val	Asp
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Leu	Ala	Thr	Leu	Met	Asn	Thr	Ile	Glu	Gln	Leu	Gly	Leu	Phe	Glu	
			265		270				275			280			
Tyr	Thr	Leu	Asp	Asn	Val	Thr	Ala	Val	Tyr	Arg	Ser	Glu	Thr	Ala	Arg
			285			290				295					
Thr	Thr	Gly	Asp	Ile	Ala	Arg	Val	Pro	Val	Leu	Val	Gly	Thr	Val	Ala
			300			305				310					
Asn	Asp	Gly	Leu	Leu	Phe	Val	Leu	Gly	Glu	Asn	Asp	Thr	Gln	Ala	Tyr
			315			320				325					
Leu	Glu	Glu	Ala	Ile	Pro	Asn	Gln	Pro	Asp	Leu	Tyr	Gln	Thr	Leu	Leu
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Gly	Ala	Tyr	Pro	Ile	Gly	Ser	Pro	Gly	Ile	Gly	Ser	Pro	Gln	Asp	Gln
			345		350				355			360			
Ile	Ala	Ala	Ile	Glu	Thr	Glu	Val	Arg	Phe	Gln	Cys	Pro	Ser	Ala	Ile
			365			370				375					
Val	Ala	Gln	Asp	Ser	Arg	Asn	Arg	Gly	Ile	Pro	Ser	Trp	Arg	Tyr	Tyr
			380			385				390					
Tyr	Asn	Ala	Thr	Phe	Glu	Asn	Leu	Glu	Leu	Phe	Pro	Gly	Ser	Glu	Val
			395			400				405					
Tyr	His	Ser	Ser	Glu	Val	Gly	Met	Val	Phe	Gly	Thr	Tyr	Pro	Val	Ala
			410			415				420					
Ser	Ala	Thr	Ala	Leu	Glu	Ala	Gln	Thr	Ser	Lys	Tyr	Met	Gln	Gly	Ala
			425		430				435			440			
Trp	Ala	Ala	Phe	Ala	Lys	Asn	Pro	Met	Asn	Gly	Pro	Trp	Lys	Gln	
			445			450				455					
Val	Pro	Asn	Val	Ala	Ala	Leu	Gly	Ser	Pro	Gly	Lys	Ala	Ile	Gln	Val
			460			465				470					
Asp	Val	Ser	Pro	Ala	Thr	Ile	Asp	Gln	Arg	Cys	Ala	Leu	Tyr	Thr	Arg
			475			480				485					
Tyr	Tyr	Thr	Glu	Leu	Gly	Thr	Ile	Ala	Pro	Arg	Thr	Phe	Gly	Gly	Gly
			490			495				500					
Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Lys	Asp	Asn	Val	Ala	Asp	Val	
			505			510				515			520		
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
			525			530				535					
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Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr
		585					590				595			600	
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
		605						610					615		
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala
		620						625				630			
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln
		635						640				645			
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe
		650						655				660			
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val
		665					670				675			680	
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile
		685						690				695			
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser
		700						705				710			
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys
		715						720				725			
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro
		730						735				740			
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala
		745					750				755			760	
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys
		765						770				775			
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe
		780						785				790			
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile
		795						800				805			
Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp
		810					815				820				
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile
		825					830				835			840	
Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile
		845						850				855			
Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser
		860						865				870			
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		875						880				885			
Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile
		890					895				900				
Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr
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		925						930				935			
Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly
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Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val
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<212> DNA

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<223> Barley alpha amylase signal sequence: BEST1
 mature: artificial spacer: and K:trAPAO. For
 plant expression.

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 <223> Barley alpha amylase signal sequence.

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Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr		
-5	1	5

gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc	144	
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg		
10	15	20

gga ata ccc tat gca gcg ccg cgg gtg ggc ggg ctg cgt tgg aag ccg	192	
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25	30	40

ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt	240	
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe		
45	50	55

ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc	288	
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala		
60	65	70

ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca	336	
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser		
75	80	85

ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc	384	
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly		
90	95	100

ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg	432
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala	

105	110	115	120	
ctt gcg cga cag ggc gtc gtc gtg acg ttt aac tat cgg acg aac Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn 125	130	135		480
atc ctg ggc ttt ttc gcc cat cct ggt ctc tgc cgc gag agc ccc acc Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr 140	145	150		528
gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg 155	160	165		576
tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Asp Pro Gly Arg Val 170	175	180		624
acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu 185	190	195	200	672
acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser 205	210	215		720
cca ggg ctg acg cga ccg ctc gcg acg ctc gac agc gcc gcc tcg Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser 220	225	230		768
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro 235	240	245		816
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp 250	255	260		864
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu 265	270	275	280	912
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val 285	290	295		960
cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly 300	305	310		1008
cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala 315	320	325		1056
cag ttt ggc gac caa gcc gcc gtc gtg gcg gcg tgc tat ccc ctc gac Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp 330	335	340		1104
ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn 345	350	355	360	1152

cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln 365	370	375	1200
ggc gcg ccc gtc tgg cgt tat cag ttc aac ggt aat acc gag ggt gga Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly 380	385	390	1248
aga gcg ccc gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtc Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val 395	400	405	1296
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccc gag ggg ccc Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro 410	415	420	1344
acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val 425	430	435	1392
cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro 445	450	455	1440
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg 460	465	470	1488
gcg gcg gtc gtc ccc gga cct tcc atc ccc cct tgc gcg gat ggc Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly 475	480	485	1536
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc Ala Lys Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser 490	495	500	1584
aaa gac aac gtt gcg gac gtc gta gtg gtg ggc gct ggc ttg agc ggt Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly 505	510	515	1632
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val 525	530	535	1680
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 540	545	550	1728
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 555	560	565	1776
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 570	575	580	1824
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 585	590	595	1872
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu			1920

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gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	620	625	630	1968
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	635	640	645	2016
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	650	655	660	2064
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	665	670	675	2112
gtt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	685	690	695	2160
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	700	705	710	2208
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	715	720	725	2256
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	730	735	740	2304
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	745	750	755	2352
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Val Val Val Ser Leu Pro Thr Thr	765	770	775	2400
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	780	785	790	2448
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	795	800	805	2496
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	810	815	820	2544
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	825	830	835	2592
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	845	850	855	2640

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 860 865 870	2688
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 875 880 885	2736
ccg gcc aac gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 890 895 900	2784
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 905 910 915 920	2832
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acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 940 945 950	2928
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 955 960 965	2973
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Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg 10 15 20	
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro 25 30 35 40	
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe 45 50 55	
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala 60 65 70	
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser 75 80 85	
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly 90 95 100	
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala 105 110 115 120	
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn 125 130 135	
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr 140 145 150	

Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg
 155 160 165
 Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val
 170 175 180
 Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu
 185 190 195 200
 Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser
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 Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser
 220 225 230
 Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro
 235 240 245
 Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp
 250 255 260
 Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu
 265 270 275 280
 Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val
 285 290 295
 Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly
 300 305 310
 Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala
 315 320 325
 Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp
 330 335 340
 Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn
 345 350 355 360
 Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln
 365 370 375
 Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly
 380 385 390
 Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val
 395 400 405
 Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro
 410 415 420
 Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val
 425 430 435 440
 Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro
 445 450 455
 Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg
 460 465 470
 Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly
 475 480 485
 Ala Lys Ala Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser
 490 495 500
 Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly
 505 510 515 520
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 525 530 535
 Leu Glu Ala Met Asp Arg Val Gly Lys Thr Leu Ser Val Gln Ser
 540 545 550
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
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 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
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 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
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 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
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 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
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 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 635 640 645

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
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 665 670 675 680
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 685 690 695
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
 700 705 710
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
 715 720 725
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
 730 735 740
 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
 745 750 755 760
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
 765 770 775
 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 780 785 790
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 795 800 805
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 810 815 820
 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 825 830 835 840
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 845 850 855
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 860 865 870
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 875 880 885
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 890 895 900
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 905 910 915 920
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 925 930 935
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<212> DNA

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<220>

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polylinker; 688-2190, esp1 mat; 2191-2226 spacer;
2227-3615, K:trAPAO, extra lysine; 3616-3618, stop
codon. For bacterial expression.

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<222> (1)...(687)

<223> gast + polylinker

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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
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Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
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Met Leu Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
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Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
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aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
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Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
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Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
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Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	

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gac tgc ctg aac ctc aac atc tac gtc cca gga act gag aac aca aac Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn 325 330 335	1008
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gtc atc gcc gtg acc atc aac tac aga acg aac att ctg ggg ttc cct Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro 370 375 380	1152
gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg ttc cta gac Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp 385 390 395 400	1200
caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca gcc ttt ggc Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly 405 410 415	1248
ggg gat cct cga aag gtc aca ata ttt ggg cag agt gcg ggg ggc aga Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg 420 425 430	1296
agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca ccc ttc cga Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg	1344

435	440	445	
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gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc aac tgt acc Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr 465	470	475	1440
acc agt atc gac atc ttg agt tgt atg aga aga gtc gat ctc gcc act Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr 485	490	495	1488
ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag tac acg ttg Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu 500	505	510	1536
gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc acg act ggt Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly 515	520	525	1584
gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc aac gac gga Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly 530	535	540	1632
ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat ctc gag gag Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu 545	550	555	1680
gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt gga gca tat Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr 565	570	575	1728
ccc att gga tcc cca ggg atc gga tcg cct caa gat cag att gcc gcc Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala 580	585	590	1776
att gag acc gag gta aga ttc cag tgt cct tct gcc atc gtg gct cag Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln 595	600	605	1824
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acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser 625	630	635	1920
tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gcg acc Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr 645	650	655	1968
gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala 660	665	670	2016
ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa gtg ccg aat Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn 675	680	685	2064

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cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt tat tat act Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr 705 710 715 720	2160
gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc agc ggc gga Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Ser Gly Gly 725 730 735	2208
ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val 740 745 750	2256
ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala 755 760 765	2304
ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys 770 775 780	2352
act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu 785 790 795 800	2400
ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu 805 810 815	2448
ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn 820 825 830	2496
tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly 835 840 845	2544
gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu 850 855 860	2592
ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys 865 870 875 880	2640
gcg agc cct caq gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr 885 890 895	2688
tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln 900 905 910	2736
atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu 915 920 925	2784
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930	935	940	
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cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val 965 970 975			2928
cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys 980 985 990			2976
aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val 995 1000 1005			3024
gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro 1010 1015 1020			3072
ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr 1025 1030 1035 1040			3120
tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln 1045 1050 1055			3168
ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala 1060 1065 1070			3216
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atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val 1090 1095 1100			3312
cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala 1105 1110 1115 1120			3360
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gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val 1155 1160 1165			3504
cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu 1170 1175 1180			3552

ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc
 Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser
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 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val
 225 230 235 240
 Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu
 245 250 255
 Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro
 260 265 270
 Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly
 275 280 285
 Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile
 290 295 300
 Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu
 305 310 315 320
 Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn
 325 330 335
 Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp
 340 345 350
 Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp
 355 360 365
 Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro

370	375	380
Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp		
385	390	395
Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly		400
405	410	415
Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg		
420	425	430
Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg		
435	440	445
Ala Ala Ile Met Glu Ser Gly val Ala Asn Tyr Asn Phe Pro Lys Gly		
450	455	460
Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr		
465	470	475
Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr		480
485	490	495
Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu		
500	505	510
Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly		
515	520	525
Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly		
530	535	540
Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu		
545	550	555
Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr		560
565	570	575
Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala		
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Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln		
595	600	605
Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala		
610	615	620
Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser		
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Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr		
645	650	655
Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala		
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Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn		
675	680	685
Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser		
690	695	700
Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr		
705	710	715
Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Ser Gly Gly		
725	730	735
Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val		
740	745	750
Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala		
755	760	765
Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys		
770	775	780
Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu		
785	790	795
Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu		800
805	810	815
Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn		
820	825	830
Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly		
835	840	845
Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu		
850	855	860
Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys		

865	870	875	880
Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr			
885	890	895	
Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln			
900	905	910	
Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu			
915	920	925	
Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe			
930	935	940	
Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met			
945	950	955	960
Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val			
965	970	975	
His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys			
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Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val			
995	1000	1005	
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro			
1010	1015	1020	
Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr			
1025	1030	1035	1040
Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln			
1045	1050	1055	
Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala			
1060	1065	1070	
Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe			
1075	1080	1085	
Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val			
1090	1095	1100	
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala			
1105	1110	1115	1120
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser			
1125	1130	1135	
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn			
1140	1145	1150	
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val			
1155	1160	1165	
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu			
1170	1175	1180	
Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser			
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Leu Val Pro Ala Ala			
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<212> DNA

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<220>

<223> Open reading frame of BEST1:K:trAPAO fusion for bacterial expression vector pGEX-4T-1 or similar vector.
gst:BEST1:sp:K:trAPAO fusion, 3591 nt. 1-687 gst + polylinker, 688-2163, BEST1 mature; 2164-2199, spacer, 2200-3588, K:trAPAO

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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
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Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	

gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr 180 185 190	576
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205	624
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220	672
gga tcc ccg gaa ttc acg gat ttt ccg gtc cgc agg acc gat ctg ggc Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly 225 230 235 240	720
cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc gga ata ccc Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro 245 250 255	768
tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg ccc caa cac Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His 260 265 270	816
gcc cgccccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt ggc tcc gac Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp 275 280 285	864
tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc ccc ggc gtg Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val 290 295 300	912
agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca ggc gct aaa Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys 305 310 315 320	960
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agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg acg gtc ttt Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe 405 410 415	1248
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Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro			
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Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu			
435	440	445	
acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg ggc gag cgc			1392
Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg			
450	455	460	
ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca gcc acc ctg			1440
Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu			
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Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg			
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Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn			
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Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro			
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Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly Arg Ala Pro			
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gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg ttc aag ctc			1920
Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu			
625	630	635	640
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Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala			
645	650	655	
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Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala			
660	665	670	

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gca cgc aaa gtc cag gcc ggc ggt ctg tcc tgc ctc gtt ctt gag gcg Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala 755 760 765	2304
atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly 770 775 780	2352
agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn 785 790 795 800	2400
caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu 805 810 815	2448
ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt aca Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr 820 825 830	2496
acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala 835 840 845	2544
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cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp 865 870 875 880	2640
agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala 885 890 895	2688
gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu 900 905 910	2736
gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc	2784

Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala			
915	920	925	
acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat			2832
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr			
930	935	940	
atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag			2880
Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys			
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gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att			2928
Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile			
965	970	975	
gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg			2976
Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val			
980	985	990	
ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc			3024
Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro			
995	1000	1005	
acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg			3072
Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala			
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gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac			3120
Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp			
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aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc			3168
Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser			
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tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga			3216
Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg			
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caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cg aag tgg			3264
Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp			
1075	1080	1085	
tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc			3312
Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu			
1090	1095	1100	
cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac			3360
Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn			
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gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg			3408
Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro			
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agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc			3456
Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu			
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aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta			3504
Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu			
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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu			
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Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys			
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Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn			
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Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu			
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Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser			
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Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu			
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Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn			
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Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp			
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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu			
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Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr			
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Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala			
195	200	205	
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg			
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Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly			
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Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro			
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Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His			
260	265	270	
Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp			
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Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val			
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Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys			
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Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Phe Ala			
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Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg			
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Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly			

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Gly	Asn	Tyr	Gly	Leu	Leu	Asp	Ile	Leu	Ala	Ala	Leu	Arg	Trp	Val	Gln
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Ser	Asn	Ala	Arg	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Arg	Val	Thr	Val	Phe
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Gly	Glu	Ser	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Leu	Leu	Leu	Thr	Ser	Pro
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Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu	Ser	Pro	Gly	Leu
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Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala	Ser	Gly	Glu	Arg
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Leu	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Arg	Ser	Thr	Asp	Pro	Ala	Thr	Leu
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Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu	Pro	Gln	Thr
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Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val	Arg	Val	Leu
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Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly	Arg	Ala	Pro
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Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala	Gln	Phe	Gly
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Asp	Gln	Ala	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp	Gly	Arg	Ala
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Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn	Gln	Phe	Asn
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Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln	Gly	Ala	Pro
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Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly	Gly	Arg	Ala	Pro
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Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly	Val	Phe	Lys	Leu
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Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	Thr	Pro	Ala
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Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val	Arg	Phe	Ala
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Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro	Ala	Tyr	Ser
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Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly	Arg	Ala	Ala	Val
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Val	Ser	Pro	Gly	Pro	Ser	Ile	Pro	Pro	Cys	Ala	Asp	Gly	Ala	Lys	Ala
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Gly	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Lys	Asp	Asn	
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Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr
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Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala
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Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly
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Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn
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Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu
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Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr
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Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala
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Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu

850	855	860
His Ser Leu Gln Asp	Leu Lys Ala Ser Pro	Gln Ala Lys Arg
865	870	875
Ser Val Ser Phe Ala His Tyr Cys	Glu Lys Glu Leu Asn	Leu Pro Ala
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Val Leu Gly Val Ala Asn Gln	Ile Thr Arg Ala	Leu Leu Gly Val Glu
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Ala His Glu Ile Ser Met	Leu Phe Leu Thr Asp	Tyr Ile Lys Ser Ala
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Thr Gly Leu Ser Asn Ile Phe Ser Asp	Lys Lys Asp	Gly Gly Gln Tyr
930	935	940
Met Arg Cys Lys Thr Gly	Met Gln Ser Ile Cys	His Ala Met Ser Lys
945	950	955
Glu Leu Val Pro Gly Ser Val His	Leu Asn Thr Pro Val	Ala Glu Ile
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Glu Gln Ser Ala Ser Gly Cys	Thr Val Arg Ser Ala	Ser Gly Ala Val
980	985	990
Phe Arg Ser Lys Lys Val Val	Val Ser Leu Pro	Thr Thr Leu Tyr Pro
995	1000	1005
Thr Leu Thr Phe Ser Pro	Pro Leu Pro Ala	Glu Lys Gln Ala Leu Ala
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Glu Asn Ser Ile Leu Gly Tyr	Tyr Ser Lys Ile Val	Phe Val Trp Asp
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Lys Pro Trp Trp Arg Glu Gln Gly	Phe Ser Gly Val	Leu Gln Ser Ser
1045	1050	1055
Cys Asp Pro Ile Ser Phe Ala Arg	Asp Thr Ser Ile Asp	Val Asp Arg
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Gln Trp Ser Ile Thr Cys Phe	Met Val Gly Asp	Pro Gly Arg Lys Trp
1075	1080	1085
Ser Gln Gln Ser Lys Gln Val	Arg Gln Lys Ser Val	Trp Asp Gln Leu
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Arg Ala Ala Tyr Glu Asn	Ala Gly Ala Gln Val	Pro Glu Pro Ala Asn
1105	1110	1115
Val Leu Glu Ile Glu Trp Ser	Lys Gln Gln Tyr	Phe Gln Gly Ala Pro
1125	1130	1135
Ser Ala Val Tyr Glu Asn Asp	Leu Ile Thr Leu Gly	Ser Ala Leu
1140	1145	1150
Arg Thr Pro Phe Lys Ser Val	His Phe Val Gly	Thr Glu Thr Ser Leu
1155	1160	1165
Val Trp Lys Gly Tyr Met	Glu Gly Ala Ile Arg	Ser Gly Gln Arg Gly
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<223> mutation in putative glycosylation site (AGC->AAC)

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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg      96
Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20          25          30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg      144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35          40          45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa      192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50          55          60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac      240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65          70          75          80

atg ttg ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa      288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85          90          95

gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt      336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100         105         110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa      384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115         120         125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat      432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130         135         140

ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat      480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145         150         155         160

gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta      528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165         170         175

gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac      576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180         185         190

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acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220	672
gga tcc ccg gaa ttc atg gca ctt gca ccg agc tac atc aat ccc cca Gly Ser Pro Glu Phe Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro 225 230 235 240	720
aac gtc gcc tcc cca gca ggg tat tct cac gtc ggc gta ggc cca gac Asn Val Ala Ser Pro Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp 245 250 255	768
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ggc gtg aca gac cct gcc tac gag aaa cag gtt gcc caa gca ttc gcc Gly Val Thr Asp Pro Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala 275 280 285	864
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aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val 465	470	475	1440
gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu 485	490	495	1488
gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu 500	505	510	1536
gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro 515	520	525	1584
gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val 530	535	540	1632
gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser 545	550	555	1680
gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln 565	570	575	1728
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ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu 645	650	655	1968
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp 660	665	670	2016
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser 675	680	685	2064

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cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cg aag Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys 705	710	715	720	2160
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln 725	730	735	2208	
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala 740	745	750	2256	
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35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp

145	150	155	160
Val Val Leu Tyr Met Asp Pro Met Cys	Leu Asp Ala Phe Pro Lys	Leu	
165	170	175	
Val Cys Phe Lys Lys Arg Ile Glu Ala	Ile Pro Gln Ile Asp Lys	Tyr	
180	185	190	
Leu Lys Ser Ser Lys Tyr Ile Ala Trp	Pro Leu Gln Gly Trp Gln	Ala	
195	200	205	
Thr Phe Gly Gly Asp His Pro Pro Lys	Ser Asp Leu Val Pro Arg		
210	215	220	
Gly Ser Pro Glu Phe Met Ala Leu Ala	Pro Ser Tyr Ile Asn Pro	Pro	
225	230	235	240
Asn Val Ala Ser Pro Ala Gly Tyr Ser	His Val Gly Val Gly	Pro Asp	
245	250	255	
Gly Gly Arg Tyr Val Thr Ile Ala Gly	Gln Ile Gly Gln Asp Ala	Ser	
260	265	270	
Gly Val Thr Asp Pro Ala Tyr Glu Lys	Gln Val Ala Gln Ala Phe	Ala	
275	280	285	
Asn Leu Arg Ala Cys Leu Ala Ala Val	Gly Ala Thr Ser Asn Asp	Val	
290	295	300	
Thr Lys Leu Asn Tyr Tyr Ile Val Asp	Tyr Ala Pro Ser Lys Leu	Thr	
305	310	315	320
Ala Ile Gly Asp Gly Leu Lys Ala Thr	Phe Ala Leu Asp Arg Leu	Pro	
325	330	335	
Pro Cys Thr Leu Val Pro Val Ser Ala	Leu Ser Ser Pro Glu Tyr	Leu	
340	345	350	
Phe Glu Val Asp Ala Thr Ala Leu Val	Pro Gly His Thr Thr Pro Asp		
355	360	365	
Asn Val Ala Asp Val Val Val Gly	Ala Gly Leu Ser Gly Leu	Glu	
370	375	380	
Thr Ala Arg Lys Val Gln Ala Ala Gly	Leu Ser Cys Leu Val Leu	Glu	
385	390	395	400
Ala Met Asp Arg Val Gly Gly Lys	Thr Leu Ser Val Gln Ser Gly	Pro	
405	410	415	
Gly Arg Thr Thr Ile Asn Asp Leu Gly	Ala Ala Trp Ile Ser Asp	Ser	
420	425	430	
Asn Gln Asn Glu Val Ser Arg Leu Phe	Glu Arg Phe His Leu Glu	Gly	
435	440	445	
Glu Leu Gln Arg Thr Thr Gly Asn Ser	Ile His Gln Ala Gln Asp	Gly	
450	455	460	
Thr Thr Thr Ala Pro Tyr Gly Asp Ser	Leu Leu Ser Glu Glu	Val	
465	470	475	480
Ala Ser Ala Leu Ala Glu Leu Leu Pro	Val Trp Ser Gln Leu	Ile Glu	
485	490	495	
Glu His Ser Leu Gln Asp Leu Lys Ala	Ser Pro Gln Ala Lys Arg	Leu	
500	505	510	
Asp Ser Val Ser Phe Ala His Tyr Cys	Glu Lys Glu Leu Asn Leu	Pro	
515	520	525	
Ala Val Leu Gly Val Ala Asn Gln Ile	Thr Arg Ala Leu Leu Gly	Val	
530	535	540	
Glu Ala His Glu Ile Ser Met Leu Phe	Leu Thr Asp Tyr Ile Lys	Ser	
545	550	555	560
Ala Thr Gly Leu Ser Asn Ile Phe Ser	Asp Lys Lys Asp Gly	Gly Gln	
565	570	575	
Tyr Met Arg Cys Lys Thr Gly Met Gln	Ser Ile Cys His Ala Met	Ser	
580	585	590	
Lys Glu Leu Val Pro Gly Ser Val His	Leu Asn Thr Pro Val Ala	Glu	
595	600	605	
Ile Glu Gln Ser Ala Ser Gly Cys Thr	Val Arg Ser Ala Ser Gly	Ala	
610	615	620	
Val Phe Arg Ser Lys Lys Val Val Val	Ser Leu Pro Thr Thr Leu	Tyr	
625	630	635	640
Pro Thr Leu Thr Phe Ser Pro Pro Leu	Pro Ala Glu Lys Gln Ala	Leu	